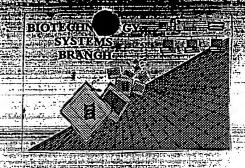
RAWSEQUENCELISTING



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/622, 206

Source: PCT 09

Date Processed by STIC: 1/1/200/

Date Processed by STIC:

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS. PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE

APPLICANT, WITH A NOTICE TO COMPLY or,

TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216. PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax) PATENTIN 3.0 e-mail help: patin30help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2Kcompliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address: http://www.uspto.gov/web/offices/pac/checker

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/622,206

•	_ Wrapped Nucleics	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it.								
		Please adjust your right margin to .3, as this will prevent "wrapping".								
2	Wrapped Aminos	The amino acid number/text at the end of each line "wrapped " down to the next line.								
		This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping".								
3	Incorrect Line Length	The rules require that a line not exceed 72 characters in length. This includes spaces.								
4	Misaligned Amino Acid	The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs								
	Numbering	between the numbering. It is recommended to delete any tabs and use spacing between the numbers.								
5	Non-ASCII	This file was not saved in ASCII (DOS) lext, as required by the Sequence Rules.								
		Please ensure your subsequent submission is saved in ASCII text so that it can be processed.								
6	Variable Length	Sequence(s) contain n's or Xaa's which represented more than one residue.								
		As per the rules, each n or Xaa can only represent a single residue.								
		Please present the maximum number of each residue having variable length and								
		indicate in the (ix) feature section that some may be missing.								
7	Patentin ver. 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid								
		sequence(s) Normally, Patentin would automatically generate this section from the								
		previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223>								
		sections for Artificial or Unknown sequences.								
8	Skipped Sequences	Sequence(s) missing. If intentional, please use the following format for each skipped sequence:								
	(OLD RULES)	(2) INFORMATION FOR SEQ ID NO:X:								
		(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")								
		(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:								
		This sequence is intentionally skipped								
		Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).								
9	Skipped Sequences	Sequence(s) missing. If intentional, please use the following format for each skipped sequence.								
	(NEW RULES)	<210> sequence id number								
		\$400> sequence id number								
		000								
<u></u>	Use of n's or Xaa's	Use of n's and/or Xaa's have been detected in the Sequence Listing.								
	(NEW RULES)	Use of <220> to <223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.								
1	Use of <213>Organism	Sequence(s) are missing this mandatory field or its response.								
	(NEW RULES)									
2	Use of <220>Feature	Sequence(s) are missing the <220>Feature and associated headings.								
	(NEW RULES)	Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"								
	•	Please explain source of genetic material in <220> to <223> section.								
		(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules								
з	Patentin ver. 2.0 "bug"	Please do not use "Copy to Disk" function of Patentin version 2.0. This causes a corrupted								
	District of the same of	File, Testitling in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).								

PCT09

```
Does Not Comply
                                                                                           Corrected Diskette Needed
                      Imput Set : A:\400683seqlist.txt
                     Output, Set: N:\CRF3\01112001\1622206.raw
      4 <110> APPLICANT: Laboratory of Molecular Biophotonics
      6 81205 TITLE OF INVENTION: Mothod for quantilatively detecting entires
      8 KL30> FINE REPERENCE: F930-0008-00
   > 10 <140 > CUPRENT APPLICATION NUMBER: US/09/622,206
    11 <141> CURRENT FILING DATE: 2000-08-14
     13 <160> NUMBER OF SEQ 10 NOS: 13
     15 -170> SOFTWARE: Patentin Ver. 2.1
     17 - 210 > SEQ ID NQ: i
     18 4243> DESSTE: 23
     19 <212> TYPE: DNA
     20 <213> ORGANISM: Artificial Sequence
     22 -220> FEATURE:
     23 <223> OTHER INFORMATION: Primer
     25 <100> SEQUENCE: 1
                                                                              23
     26 saggismare igeogsagic wgg
     29 <210> SEG ID NO: 2
     30 <211> bfMGTB: 34
     31 <212> TYPE: DNA
     32 <213> ORGANISM: Artificia: Sequence
     34 <220> FEATURE:
     35 <223> OTHER INFORMATION: Primer
     37 <400> SEQUENCE: 2
                                                                              34
     38 gegleafeta gaacaacean aatheotiggg caca
     41 <210> SEQ ID NO: 3
     41 <211> LENGTH: 32
     43 <212> TYPE: DNA
     44 <213> ORGAMISM: Artificial Sequence
     17 <2235 OTHER THEORIAN CON: Primer see them 10 on Eva Jumpay Sheet
49 <4005 SEQUENCE: 3
50 CCAGNESYDA GCCCSWIMES AND AND OF
w--> 50 ccagwtsyga gctcswints adhcagnindy ch
53 <210> SEQ'ID NO: 4
54 <211> LENGTH: 21
     55 <212> TYPE: DNA
     56 <213> ORGANISM: Artificial Sequence
     58 <220> FEATURE:
     59 <223> OTHER INFORMATION: Primer
     61 <400> SEQUENCE: 4
                                                                              21.
     62 acadecatto otgettgaage t
     65 <210> SEQ ID NO: 5
     66 <213> LENGTH: 23
     67 <212> TYPE: DNA
     68 <213> ORGANISM: Artificial Sequence
     70 <220> FEATURE:
     71 <223> OTHER INFORMATION: Primer
     73 <400> SEQUENCE: 5
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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/622,206

DATE: 01/11/2001

23

TIME: 17:19:13

74 saggismare tgeagsagic wgg

RAW SEQUENCE LISTING

DATE: 01/11/2001

PATENT APPLICATION: US/09/622,206

TIME: 17:19:13

Input Set : A:\400683seqlist.txt
Output Set: N:\CRF3\01112001\1622206.raw

```
77 <210> SEQ ID NO: 6
78 -.211> LENGTH: 33
79 <212> TYPE: DNA
30 <213> ORGANISM: Aprificial Sequence
83 K2200 FEATURE:
83 <223> OTHER INFORMATION: Primer
35 <400> SEQUENCE: 6
35 getygadagg gatedagagt edeaggtdad tgt.
                                                                     3.3
89 <210> SEO LD NO: 7
96 <211> LENGTH: 57
91 SELL TYPE: DNA
32 <213> ORGANISM: Actificial Sequence
94 <220> FEATURE:
95 <223> OTHER INFORMATION: Primer
97 +400> SEQUENCE: 7
98 catgrigact gactogocc ageogocat goccanque cagetocage agreege
101 <210> SEO ID NO: 8
102 <211> LENGTH: 48
103 <212> TYPE: DNA
104 <213> ORGANISM: Artificial Sequence
106 <220> FEATURE:
107 <223> OTHER INFORMATION: Primer
109 <400> SEQUENCE: 8
110 ccacquitet geggeegeac acteaticet gitgaagete titgiaat
113 <210> SEQ 1D NO: 9
114 <211> LENGTH: 106
115 k213> TYPE: PRT
116 <213> ORGANISM: Mouse
118 <400> SEQUENCE: 9
119 Ala Lys Thr Thi Pro Pro Ser Val Tyr Pro Leu Ala Pro Gly Ser Ala
120 1
                     -5
                                        10
122 Ala Glm Thr Asn Ser Met Val Thr Leu Gly Cys Leu Val Lys Gly Tyr
               20
                                    25
                                                         3.0
123
125 Phe Pro Glu Pro Val Thr Val Thr Trp Asp Ser Gly Ser Leu Ser Ser
126
        3.5
                                4.0
                                                    . 45
128 Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu
129
       50
                            5.5
                                                6.0
131 Ser Ser Ser Val Thr Val Pro Ser Ser Thr Trp Pro Ser Cle Thi Val
132 65
                        741
                                            7.5
                                                                86
134 Thr Cys Asn Val Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys
                    85
                                        90
137 Ile Val Pro Arg Asp Cys Gly Cys Ser Arg
                                 105
138
             100
141 <210> SEQ TD NO: 10
142 <211> LENGTH: 106
143 <212> TYPE: PRT
144 <213> ORGANISM: Mouse
146 <400> SEQUENCE: 10
147 Ala Lys Thr Thr Pro Pro Ser Val Tyr Pro Leu Ala Pro Gly Ser Ala
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 RAW SEQUENCE LISTING
 DATE: 01/41/2001

 PATENT APPLICATION: US/09/622,206
 TIME: 17:19:13

input Set: A:\400683seqlist.txt
Output Set: N:\CRF3\01112001\1622206.raw

```
148
                                        10
150 Ala Gin Thr Ash Ser Met Val Thr Leu Gly Cys Leu Val Lys Gly Tyr
            20
                                    25
153 Phe Pro Chu Pro Val The val Thr Try Ash Ser Chy Ser ion Ser Ser
         3.5
176 Cly Var his the Pho Pro Ata Val Lou Glm Ser Asp Lou tyr The Lou
157 50
159 Ser Ser Ser Val Thr Val Pro Ser Ser Thr Trp Pro Ser Glu Thr Val
160 65
162 Thr Cys Ash Val Ala Bis Pro Ala Ser Ser Thr Lys Val Asp Lys Lys 163 -90 -85
145 The Val Pro Arg Asp Cvs Gly Cys Ser Arg
            106
166
169 <210> SEQ JO NO: 11
170 .211. HENOTH: 86
171 3212> TYPE: ONA
172 <21 >> OMGANISM: Artificial Sequence
174 <220> FEATURE:
175 .223> OTHER INFORMATION: Primer
177 <400> SEQUENCE: 11
178 aggrandade edecagagaen gatetactig glegaetigg togactuags etagaaggae of
179 grigaacacte arroctiffing dagore
182 <210> SEG ID NO: 12
183 <211> LENGTH: 121
184 <212> TYPE: PRT
145 <214> ORGANISM: Mouse
187 <400> STQUENCE: 12
188 Ala Asp Ala Ala Pro Thr Val Ser Tie Phe Pro Pro Ser Ser Glu Glu
189 1
191 Len Phr Ser Gly Gly Ala Ser Val Val Cys Phe Len Ash Ash Phe Tyr
164 Pro Lys Asp the Ash Val Lys Tro Lys The Asp Cly Ser Giu Arq Gin
195 - 35 - 40 - 45
197 Ash Gir Val Led Ash Ser Trp Thr Asp Gin Asp Ser Lys Asp Ser Thr
       50
                            55
200 Tyr Ser Met. Ser Sec Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu Arg
201 65 70 75 80
203 His Ash Ser Tyr Thr Cys Glu Ala Thr His Lys Thr Ser Thr Sei Pro
                    8.5
                                        90
204
206 lle Thr Lys Ser Phe Asn Arg Asn Glu Cys Ser Arg Pro Ser Arg Pro
207
             100
                                105
209 Ser Arg Pro Ser Arg Pro Ser Arg Pro
           115
210
                      . 120
213 <216> SEQ TD NO: 13
214 <211> LENGTH: 106
215 <212> TYPE: PRT
216 <213> OPGANISH: Mouse
218 <400> SEQUENCE: 13
219 Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Glu Gin
```

RAW SEQUENCE LISTING PATENT APPLICATION: US/09/622,206

BATE: 01/11/2001 FIME: 17:19:13

Input Set : A:\400683seqlist.txt
Ontput Set: N:\CRF3\01112001\1622206.raw

220	1				5					10					1.5	
222	Leu	Thr	Ser	Gly	Gly	A1a	Sec	Val	Va I	Cys	Pho	Lou	Asn	ASH	Pho	Tyr
223				3:0					25					30		
225	Pro	1.78	Asp	ude	Asn	val	LVS	rap	Lys	13.65	Asp	C_{ij}	Sex	$G\ln n$	PTG	Glu
226			3.5					4.0					15			
228	ASU	Gly	Val	Leu	$\mathbf{A}\mathbf{S}\mathbf{H}$	Ser	1xp	the	ASP	GEn	A.S 51	$S\oplus \Gamma$	tr/s	$_{ESP}$	ser	Thr
225		3.0					5.5					50				
0.34	Tyr	$S \oplus \Gamma$	510 T	Set	ser	The	Lou	Thr	1.00	Thr	Lys	ASP	G1 u	19r	GLu	Arg
232	6.5					70					7.5					87
534	His	Asn	Ser	Tyr	This	Cys	Glu	A.1a	Ther	His	L/S	Thr	Ser	Har	Ser	Pro
235					85					0.0					95	
2:17	Lie	Thr	Lys	$S \in \Gamma$	Phy	Asn	arg	Asn	Clu	Cys						
233				100					105							
242	1/10	;														

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/622,206

DATE: 01/11/2001 TIME: 17:19:14

Imput Set : A:\400683seqlist.txt

Our put Set: N:\CRF3\01112001\1622206.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application Number L:11 H:271 C: Current Piling Date differs, Replaced Current Filing Date 1:50 M:258 W: Mandatory Feature missing, <2212 not found for SEQ ID7:3 1.50 M:258 W: Mandatory Feature missing, <2222 not found for SEQ ID7:3 L:30 M:340 W: (46) "n" or "Xua" used: Feature required, for SEQ ID#:3